

10062857

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Term:

l1 and (random near5 primer\$1 near5 region\$1)

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<u>L3</u>	l1 and (random near5 primer\$1 near5 region\$1)	1	<u>L3</u>
<u>L2</u>	L1 and random hexamer\$1	11	<u>L2</u>
<u>L1</u>	transcrib\$7 near5 RNA polymerase near5 cDNA	75	<u>L1</u>

END OF SEARCH HISTORY

10062857

=> s random (10A) primer (10a) (ynthesi#### or produc###) RNA
MISSING OPERATOR RODUC###) RNA
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s random (10A) primer# (10a) (synthesi#### or produc###) (10a)RNA
L11 83 RANDOM (10A) PRIMER# (10A) (SYNTHESI#### OR PRODUC###) (10A) RNA

=> s l11 and promoter ans RNA polymerase#
L12 0 L11 AND PROMOTER ANS RNA POLYMERASE#

=> s l11 and promoter# and RNA polymerase#
L13 1 L11 AND PROMOTER# AND RNA POLYMERASE#

=> d l13 bib ab kwic

L13 ANSWER 1 OF 1 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1991:478216 BIOSIS
DN PREV199192111976; BA92:111976
TI EXPRESSION OF A GENERAL TRANSCRIPTION INITIATION FACTOR HTFIID GENE IN
NORMAL HUMAN TISSUE A QUANTITATIVE ASSAY FOR HTFIID MESSENGER RNA BASED ON
POLYMERASE CHAIN REACTION PCR.
AU WADA C [Reprint author]; OHTANI H
CS DEP CLINICAL PATHOL, SCH MED, KITASATO UNIV, 1-15-1 KITASATO, SAGAMIHARA
228, JPN
SO Japanese Journal of Electrophoresis, (1991) Vol. 35, No. 4, pp. 285-290.
CODEN: SBBKA4. ISSN: 0031-9082.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 26 Oct 1991
Last Updated on STN: 26 Oct 1991
AB A general transcription factor IID (TFIID) binds to the TATA box
promoter element and regulates the expression of most eukaryotic
genes transcribed by **RNA polymerase II** (Pol II). A
highly sensitive, specific and quantitative assay for human TFIID (hTFIID)
mRNA was developed based on polymerase chain reaction (PCR). The
distinctive points of our procedure include the use of small amount of
total cellular **RNA** (1 µg), a **random primer**
for cDNA **synthesis**, β2-microglobulin (β2M) as an
internal control and calculation of the relative value of hTFIID
transcript from 32P-incorporation of the co-amplified PCR at different
cycles. By this procedure, distribution of the hTFIID gene expression was
for the first time demonstrated in normal human tissues and the amount of
hTFIID mRNA was measured. In some tissues such as liver, fetal lung and
placenta, moderate levels of hTFIID mRNA were detected. hTFIID transcript
appeared correlated to total mRNA initiation and protein synthesis in
tissue. This quantitative PCR procedure can be applied to more extensive
studies of gene expression.
AB A general transcription factor IID (TFIID) binds to the TATA box
promoter element and regulates the expression of most eukaryotic
genes transcribed by **RNA polymerase II** (Pol II). A
highly sensitive, specific and quantitative assay for human TFIID (hTFIID)
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internal control and calculation of the relative value of hTFIID
transcript from 32P-incorporation of the co-amplified. . .

=> s l11 and hexamer#
L14 26 L11 AND HEXAMER#

=> s l14 and RNA polymerase#
L15 2 L14 AND RNA POLYMERASE#

=> d l15 1-2 bib ab kwic

L15 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN
AN 1995:865630 CAPLUS
DN 123:250816
TI Differential display of tissue-specific messenger RNAs in *Porphyra perforata* (Rhodophyta) thallus
AU Hong, Yong-Ki; Sohn, Chul Hyun; Polne-Fuller, Miriam; Gibor, Aharon
CS Department Biotechnology, National Fisheries University Pusan, Pusan, 608-737, S. Korea
SO Journal of Phycology (1995), 31(4), 640-3
CODEN: JPYLAJ; ISSN: 0022-3646
PB Phycological Society of America
DT Journal
LA English
AB Various tissue-specific markers in differentiated regions of the *Porphyra perforata* J. Agardh thallus were identified by comparing the differential display derived from the **RNA polymerase** chain reaction (RNA-PCR) with arbitrary primers. Total RNA was extracted by the LiCl-guanidinium method from six regions of differentiated thallus: male tissue, female tissue, patch tissue, vegetative dividing tissue, vegetative non-dividing tissue, and holdfast tissue. First-strand cDNA was **synthesized** by reverse transcription of total **RNA** with **random hexamers** and amplified by PCR with arbitrary **primers**. The morphol. distinct regions of the differentiated tissue revealed the presence of tissue-specific differential display of gene expression.

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L15 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
AN 1995:453764 BIOSIS
DN PREV199598468064
TI Differential display of tissue-specific messenger RNAs in *Porphyra perforata* (Rhodophyta) thallus.
AU Hong, Yong-Ki [Reprint author]; Sohn, Chul Hyun; Polne-Fuller, Miriam; Gibor, Aharon
CS Dep. Biotechnol., Natl. Fisheries Univ. Pusan, Nam-ku, Pusan, 608-737, South Korea
SO Journal of Phycology, (1995) Vol. 31, No. 4, pp. 640-643.
CODEN: JPYLAJ. ISSN: 0022-3646.
DT Article
LA English
ED Entered STN: 27 Oct 1995
Last Updated on STN: 27 Oct 1995
AB Various tissue-specific markers in differentiated regions of the *Porphyra perforata* J. Agardh thallus were identified by comparing the differential display derived from **RNA polymerase** chain reaction (RNA-PCR) with arbitrary primers. Total RNA was extracted by the LiCl-guanidinium method from six regions of differentiated thallus: male tissue, female tissue, patch tissue, vegetative dividing tissue,

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IT Miscellaneous Descriptors

GENE EXPRESSION; REGIONAL MARKERS; **RNA POLYMERASE**
CHAIN REACTION

L10 ANSWER 1 OF 3 CAPLUS COPYRIGHT 2004 ACS on STN
 AN 2003:154562 CAPLUS
 DN 138:182030
 TI Methods and kits for generating cDNA probes for use in microarrays
 IN Hjalt, Tord
 PA Curagen Corporation, USA
 SO PCT Int. Appl., 55 pp.
 CODEN: PIXXD2
 DT Patent
 LA English
 FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2003016483	A2	20030227	WO 2002-US26063	20020816
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRAI US 2001-312893P P 20010816

AB A novel method of labeling cDNA for probing oligo-based microarrays is disclosed. The polynucleotide template of interest is reverse transcribed into double-stranded cDNA using random primers that include an RNA polymerase promoter. This cDNA is then used as a template for synthesis of labeled RNA via in vitro transcription in the presence of labeled precursors.

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IT Promoter (genetic element)

RL: BSU (Biological study, unclassified); BIOL (Biological study)
 (primers hybridizing to RNA polymerase; methods and kits for generating cDNA probes for use in microarrays)

IT 9014-24-8

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
 (phage T7, phage T3 or Sp6, primers hybridizing to promoters of; methods and kits for generating cDNA probes for use in microarrays)

L10 ANSWER 2 OF 3 MEDLINE on STN DUPLICATE 1

AN 97411082 MEDLINE

DN PubMed ID: 9266104

TI Expression of the prolactin gene in normal and neoplastic human breast tissues and human mammary cell lines: promoter usage and alternative mRNA splicing.

AU Shaw-Bruha C M; Pirruccello S J; Shull J D

CS Eppler Institute for Research in Cancer and Allied Diseases, Department of Biochemistry and Molecular Biology, University of Nebraska Medical Center, Omaha 68198-6805, USA.

NC CA-36727 (NCI)

CA-68529 (NCI)

HD-24189 (NICHHD)

SO Breast cancer research and treatment, (1997 Jul) 44 (3) 243-53.

Journal code: 8111104. ISSN: 0167-6806.

CY Netherlands

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

OS GENBANK-U75583

EM 199710

ED Entered STN: 19971013

Last Updated on STN: 19990129

Entered Medline: 19971002

AB Prolactin (PRL) has been implicated in the development of mammary cancer in rodents and humans. Although PRL and its mRNA have been detected in breast tissues and some mammary cell lines, the role of PRL as an autocrine/paracrine growth factor within the breast is not clear. A second, more distal, **promoter** has recently been identified in the human PRL gene. We have used reverse transcription-polymerase chain reaction (RT-PCR) to determine whether the distal or the proximal **promoter** directs expression of the PRL gene in normal and neoplastic breast tissues and in mammary cell lines. Total RNA was isolated from 10 normal and 20 neoplastic breast tissue samples and from 8 mammary cell lines; MDA-MB-231, SK-BR-3, T-47D, MCF10, MCF10T2, and 3 MCF7 derivatives. The RNA was reverse transcribed to cDNA using random hexamers as primers. PCR amplification of the cDNAs was performed, using a variety of PRL-specific primer pairs, and the DNA products were subjected to agarose gel electrophoresis and Southern blotting. The resulting data indicate that the PRL gene is expressed in the majority of both normal and neoplastic breast tissue samples, as well as all of the mammary cell lines. PRL-specific PCR products corresponding to transcripts that originated from the distal **promoter** were observed in a subset of the normal and neoplastic breast tissue samples and mammary cell lines. Together these data indicate that PRL transcripts in human breast tissues and human mammary cell lines originate, at least in part, from the distal PRL **promoter**. In addition, data are presented which suggest that PRL transcripts in breast tissues and mammary cell lines may undergo alternative splicing.

TI Expression of the prolactin gene in normal and neoplastic human breast tissues and human mammary cell lines: **promoter** usage and alternative mRNA splicing.

AB . . . lines, the role of PRL as an autocrine/paracrine growth factor within the breast is not clear. A second, more distal, **promoter** has recently been identified in the human PRL gene. We have used reverse transcription-polymerase chain reaction (RT-PCR) to determine whether the distal or the proximal **promoter** directs expression of the PRL gene in normal and neoplastic breast tissues and in mammary cell lines. Total RNA was isolated from 10 normal and 20 neoplastic breast tissue samples and from 8 mammary cell lines; MDA-MB-231, SK-BR-3, T-47D, MCF10, MCF10T2, and 3 MCF7 derivatives. The RNA was reverse transcribed to cDNA using random hexamers as primers. PCR amplification of the cDNAs was performed, using a variety of PRL-specific primer pairs, and the DNA products were subjected. . . as well as all of the mammary cell lines. PRL-specific PCR products corresponding to transcripts that originated from the distal **promoter** were observed in a subset of the normal and neoplastic breast tissue samples and mammary cell lines. Together these data. . . PRL transcripts in human breast tissues and human mammary cell lines originate, at least in part, from the distal PRL **promoter**. In addition, data are presented which suggest that PRL transcripts in breast tissues and mammary cell lines may undergo alternative. . .

CT . . .
Cloning, Molecular

DNA, Complementary: CH, chemistry

Gene Expression

Molecular Sequence Data

Polymerase Chain Reaction
*Prolactin: GE, genetics
Prolactin: ME, metabolism
*Promoter Regions (Genetics)
*RNA, Messenger: AN, analysis

CN 0 (DNA, Complementary); 0 (RNA, Messenger)

L10 ANSWER 3 OF 3 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
on STN

AN 97081758 EMBASE

DN 1997081758

TI Multiprimed cDNA synthesis followed by PCR is the most suitable method for
Epstein-Barr virus transcript analysis in small lymphoma biopsies.

AU Brink A.A.T.P.; Oudejans J.J.; Jiwa M.; Walboomers J.M.M.; Meijer
C.J.L.M.; Van den Brule A.J.C.

CS A.J.C. Van den Brule, Section of Molecular Pathology, Department of
Pathology, Vrije Universiteit Hospital, De Boelelaan 1117, 1081 HV
Amsterdam, Netherlands

SO Molecular and Cellular Probes, (1997) 11/1 (39-47).

Refs: 30

ISSN: 0890-8508 CODEN: MCPRE6

CY United Kingdom

DT Journal; Article

FS 004 Microbiology

005 General Pathology and Pathological Anatomy

016 Cancer

022 Human Genetics

025 Hematology

LA English

SL English

AB In this study, the reverse transcriptase-polymerase chain reaction
(RT-PCR) for the reliable detection of multiple Epstein-Barr virus (EBV)
transcripts was optimized and subsequently evaluated on lymphoma
specimens. Since often only small lymphoma biopsies are available for
analysis of EBV **transcripts**, several RT-protocols to generate
cdna from multiple targets were applied. These were multi-
primer, oligo-dT primed and **random** hexamer primed cDNA
synthesis. Multi-primer cDNA synthesis appeared to be the most suitable
method for subsequent PCR analysis of EBV targets; simultaneous priming
with up to 10 specific antisense primers (for EBNA1 and 2, LMP1 and 2,
BARF0, BHRF1, BZLF1, C **promoter** activity and the **RNA**
control genes U1A and c-abl) followed by PCR showed no loss of sensitivity
compared to single-specific antisense priming. Transcripts were
specifically detected in up to one EBV-positive JY cell in a background of
50,000 EBV-negative BJAB cells, with the exception of BZLF1 and QK spliced
EBNA1 transcripts which could only be detected in 1000 and 10,000
EBV-positive cells, respectively. The analytical sensitivities of all the
primers used in PCR, including BZLF1 and QK EBNA1 primers, were 1-10
copies of cloned RT-PCR products. The multi-primed RT-PCR was evaluated on
lymphomas (n = 13). In cases with proper **RNA** quality, EBV
expression patterns found were identical to those found in previous
studies using single-primed RT-PCR assays. In conclusion, this study shows
that multi-primed RT-PCR analysis can be used efficiently for EBV
transcript analysis in small lymphoma biopsies, thereby facilitating
studies concerning the role of EBV in lymphomagenesis.

AB . . . was optimized and subsequently evaluated on lymphoma specimens.
Since often only small lymphoma biopsies are available for analysis of EBV
transcripts, several RT-protocols to generate **cdna** from
multiple targets were applied. These were multi-**primer**, oligo-dT
primed and **random** hexamer primed cDNA synthesis. Multi-primer
cDNA synthesis appeared to be the most suitable method for subsequent PCR
analysis of EBV. . . simultaneous priming with up to 10 specific
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promoter activity and the **RNA** control genes U1A and

c-abl) followed by PCR showed no loss of sensitivity compared to single-specific antisense priming. Transcripts were. . . 1-10 copies of cloned RT-PCR products. The multi-primed RT-PCR was evaluated on lymphomas (n = 13). In cases with proper **RNA** quality, EBV expression patterns found were identical to those found in previous studies using single-primed RT-PCR assays. In conclusion, this. . .

CT Medical Descriptors:

*epstein barr virus

*lymphoma

*reverse transcription polymerase chain reaction

***rna analysis**

article

controlled study

human

human cell

human tissue

nonhuman

priority journal

tumor biopsy

*complementary dna

***virus messenger rna: EC, endogenous compound**

cell nucleus antigen

primer dna